



-1-

SEQUENCE LISTING

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<120> Gamma-Conopeptides

<130> 2314-269

<140> US 10/647,519
<141> 2003-08-26

<150> US 09/210,952
<151> 1998-12-15

<150> US 60/069,706
<151> 1997-12-16

<160> 47

<170> PatentIn Ver. 2.0

<210> 1
<211> 42
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: generic formula
of gamma-conopeptides

<220>
<221> PEPTIDE
<222> (1)..(13)
<223> Xaa at residues 1, 2, 3, 4, 5, and 6 may be
des-Xaa or any amino acid; Xaa at residues 8, 9,
10, 11 and 12 may be any amino acid; Xaa at
residue 13 may be des-Xaa or any amino acid.

<220>
<221> PEPTIDE
<222> (15)..(19)
<223> Xaa at residues 15, 16, 17 and 18 may be any amino
acid; Xaa at residue 19 is Glu,
gamma-carboxyglutamate or Gln.

<220>
<221> PEPTIDE
<222> (22)..(28)
<223> Xaa at residues 22, 23 and 24 may be any amino
acid; Xaa at residue 25 may be des-Xaa or any
amino acid; Xaa at residues 27, 28 and 29 may be
any amino acid.

<220>
 <221> PEPTIDE
 <222> (30)..(42)
 <223> Xaa at residues 30, 31 and 32 may be des-Xaa or any amino acid; Xaa at residues 34, 35, 36, 37, 38, 39, 40, 41 and 42 may be des-Xaa or any amino acid.

<400> 1
 Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa
 1 5 10 15
 Xaa Xaa Xaa Cys Cys Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa
 20 25 30
 Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 35 40

<210> 2
 <211> 42
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: generic sequence of gamma-conopeptides.

<220>
 <221> PEPTIDE
 <222> (1)..(13)
 <223> Xaa at residues 1, 2, 3, 4, 5 and 6 may be des-Xaa or any amino acid; Xaa at residues 8, 9, 10, 11 and 12 may be any amino acid; Xaa at residue 13 may be des-Xaa or any amino acid.

<220>
 <221> PEPTIDE
 <222> (15)..(22)
 <223> Xaa at residues 15, 16, 17 and 18 may be any amino acid; Xaa at residue 19 is Glu, gamma-carboxyglutamate or Gln; Xaa at residue 22 is Ser or Thr.

<220>
 <221> PEPTIDE
 <222> (23)..(29)
 <223> Xaa at residues 23 and 24 may be any amino acid; Xaa at residue 25 may be des-Xaa or any amino acid; Xaa at residues 27, 28 and 29 may be any amino acid.

<220>
 <221> PEPTIDE
 <222> (30)..(42)
 <223> Xaa at residues 30, 31 and 32 may be des-Xaa or any amino acid; Xaa at residues 34, 35, 36, 37, 38, 39, 40, 41 and 42 may be des-Xaa or any amino acid.

<400> 2
 Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa
 1 5 10 15

Xaa Xaa Xaa Cys Cys Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa
 20 25 30

Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 35 40

<210> 3
 <211> 39
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: generic formula
 of gamma-conopeptides

<220>
 <221> PEPTIDE
 <222> (1)..(13)
 <223> Xaa at residue 1 is any amino acid; Xaa at
 residues 2, 3, 4, 5 and 6 may be des-Xaa or any
 amino acid; Xaa at residues 8, 9, 10, 11, 12 and
 13 may be any amino acid.

<220>
 <221> PEPTIDE
 <222> (27)..(39)
 <223> Xaa at residues 27, 28, 29, 31, 32, 33, 34, 35, 36
 and 37 may be any amino acid; Xaa at residues 38
 and 39 may be des-Xaa or any amino acid.

<220>
 <221> PEPTIDE
 <222> (15)..(19)
 <223> Xaa at residues 15, 16, 17 and 18 may be any amino
 acid; Xaa at residue 19 is Glu or
 gamma-carboxyglutamate.

<400> 3
 Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa
 1 5 10 15

Xaa Xaa Xaa Cys Cys Ser Asn Ser Cys Asp Xaa Xaa Xaa Cys Xaa Xaa
 20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 35

<210> 4
 <211> 39
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: generic
 sequence of gamma-conopeptides.

<220>
 <221> PEPTIDE
 <222> (1)..(13)
 <223> Xaa at residue 1 is any amino acid; Xaa at
 residues 2, 3, 4, 5 and 6 may be des-Xaa or any
 amino acid; Xaa at residues 8, 9, 10, 11, 12 and

13 may be any amino acid.

<220>
<221> PEPTIDE
<222> (15)..(19)
<223> Xaa at residue 15 is Ser or Thr; Xaa at residues
16, 17 and 18 may be any amino acid; Xaa at
residue 19 is Glu or gamma-carboxyglutamate.

<220>
<221> PEPTIDE
<222> (27)..(39)
<223> Xaa at residues 27, 28, 29, 31, 32, 33, 34, 35, 36
and 37 may be any amino acid; Xaa at residues 38
and 39 may be des-Xaa or any amino acid.

<400> 4
Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa
1 5 10 15
Xaa Xaa Xaa Cys Cys Ser Asn Ser Cys Asp Xaa Xaa Xaa Cys Xaa Xaa
20 25 30
Xaa Xaa Xaa Xaa Xaa Xaa Xaa
35

<210> 5
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: generic
sequence of gamma-conopeptides.

<220>
<221> PEPTIDE
<222> (1)..(6)
<223> Xaa at residues 1 and 2 may be des-Xaa or any
amino acid; Xaa at residue 3 is Asp, Glu or
gamma-carboxyglutamate; Xaa at residues 5 and 6
may be any amino acid.

<220>
<221> PEPTIDE
<222> (7)..(16)
<223> Xaa at residue 7 is Trp or 6-bromo-Trp; Xaa at
residues 9, 10, 13 and 14 may be any amino acid;
Xaa at residue 16 is Glu or
gamma-carboxyglutamate.

<220>
<221> PEPTIDE
<222> (28)..(34)
<223> Xaa at residues 28, 30, 31, 32, 33 and 34 may be
any amino acid.

<400> 5
Xaa Xaa Xaa Cys Xaa Xaa Xaa Phe Xaa Xaa Cys Thr Xaa Xaa Ser Xaa
1 5 10 15
Cys Cys Ser Asn Ser Cys Asp Gln Thr Tyr Cys Xaa Leu Xaa Xaa Xaa
20 25 30

Xaa Xaa

<210> 6
 <211> 32
 <212> PRT
 <213> Conus pennaceus

<220>
 <221> PEPTIDE
 <222> (1)..(31)
 <223> Xaa at residue 5 is Trp or 6-bromo-Trp; Xaa at residues 14 and 26 are Glu or gamma-carboxyglutamate; Xaa at residue 31 is Pro or hydroxy-Pro.

<400> 6
 Asp Cys Thr Ser Xaa Phe Gly Arg Cys Thr Val Asn Ser Xaa Cys Cys
 1 5 10 15

Ser Asn Ser Cys Asp Gln Thr Tyr Cys Xaa Leu Tyr Ala Phe Xaa Ser
 20 25 30

<210> 7
 <211> 34
 <212> PRT
 <213> Conus textile

<220>
 <221> PEPTIDE
 <222> (1)..(34)
 <223> Xaa at residues 1, 7 and 34 are Trp or 6-bromo-Trp; Xaa at residues 3 and 16 are Glu or gamma-carboxyglutamate; Xaa at residues 31 and 32 are Pro or hydroxy-Pro.

<400> 7
 Xaa Leu Xaa Cys Ser Val Xaa Phe Ser His Cys Thr Lys Asp Ser Xaa
 1 5 10 15

Cys Cys Ser Asn Ser Cys Asp Gln Thr Tyr Cys Thr Leu Met Xaa Xaa
 20 25 30

Asp Xaa

<210> 8
 <211> 39
 <212> PRT
 <213> Conus textile

<220>
 <221> PEPTIDE
 <222> (1)..(39)
 <223> Xaa at residues 1, 2, 4, 10 and 39 are Trp or 6-bromo-Trp ; Xaa at residues 19 and 31 are Glu or gamma-carboxyglutamate; Xaa at residues 34, 36 and 37 are Pro or hydroxy-Pro.

<400> 8
 Xaa Xaa Arg Xaa Gly Gly Cys Met Ala Xaa Phe Gly Leu Cys Ser Arg
 1 5 10 15

Asp Ser Xaa Cys Cys Ser Asn Ser Cys Asp Val Thr Arg Cys Xaa Leu
20 25 30

Met Xaa Phe Xaa Xaa Asp Xaa
35

<210> 9
<211> 27
<212> PRT
<213> Conus textile

<220>
<221> PEPTIDE
<222> (1)..(27)
<223> Xaa at residues 9, 13 and 17 are Glu or
gamma-carboxyglutamate.

<400> 9
Cys Lys Thr Tyr Ser Lys Tyr Cys Xaa Ala Asp Ser Xaa Cys Cys Thr
1 5 10 15

Xaa Gln Cys Val Arg Ser Tyr Cys Thr Leu Phe
20 25

<210> 10
<211> 34
<212> PRT
<213> Conus textile

<220>
<221> PEPTIDE
<222> (1)..(34)
<223> Xaa at residues 2, 3, 10 and 32 are Trp or
6-bromo-Trp; Xaa at residues 18, 26 and 33 are Glu
or gamma-carboxyglutamate; Xaa at residue 12 is
Pro or hydroxy-Pro.

<400> 10
Asp Xaa Xaa Asp Asp Gly Cys Ser Val Xaa Gly Xaa Cys Thr Tyr Asn
1 5 10 15

Ala Xaa Cys Cys Ser Gly Asp Cys His Xaa Thr Cys Ile Phe Gly Xaa
20 25 30

Xaa Val

<210> 11
<211> 31
<212> PRT
<213> Conus textile

<220>
<221> PEPTIDE
<222> (1)..(31)
<223> Xaa at residues 3 and 31 are Trp of 6-bromo-Trp;
Xaa at residues 5, 18, 22 and 25 are Glu or
gamma-carboxyglutamate; Xaa at residue 16 is Pro
or hydroxy-Pro.

<400> 11
Gly Met Xaa Gly Xaa Cys Lys Asp Gly Leu Thr Thr Cys Leu Ala Xaa

1	5	10	15
Ser Xaa Cys Cys Ser Xaa Asp Cys Xaa Gly Ser Cys Thr Met Xaa			
	20	25	30

<210> 12
 <211> 32
 <212> PRT
 <213> Conus gloriamaris

<220>
 <221> PEPTIDE
 <222> (1)..(32)
 <223> Xaa at residue 5 is Trp or 6-bromo-Trp; Xaa at residue 1 is Glu or gamma-carboxyglutamate; Xaa at residues 8 and 11 are Pro or hydroxy-Pro.

<400> 12
Xaa Cys Arg Ala Xaa Tyr Ala Xaa Cys Ser Xaa Gly Ala Gln Cys Cys
1 5 10 15
Ser Leu Leu Met Cys Ser Lys Ala Thr Ser Arg Cys Ile Leu Ala Leu
20 25 30

<210> 13
 <211> 29
 <212> PRT
 <213> Conus marmoreus

<220>
 <221> PEPTIDE
 <222> (1)..(29)
 <223> Xaa at residues 8 and 15 are Trp or 6-bromo-Trp; Xaa at residues 5, 16 and 23 are Glu or gamma-carboxyglutamate; Xaa at residue 10 is Pro or hydroxy-Pro.

<400> 13
Asn Gly Gln Cys Xaa Asp Val Xaa Met Xaa Cys Thr Ser Asn Xaa Xaa
1 5 10 15
Cys Cys Ser Leu Asp Cys Xaa Met Tyr Cys Thr Gln Ile
20 25

<210> 14
 <211> 27
 <212> PRT
 <213> Conus marmoreus

<220>
 <221> PEPTIDE
 <222> (1)..(27)
 <223> Xaa at residue 4 is Trp or 6-bromo-Trp; Xaa at residues 9, 12, 13 and 17 are Glu or gamma-carboxyglutamate.

<400> 14
Cys Gly Gly Xaa Ser Thr Tyr Cys Xaa Val Asp Xaa Xaa Cys Cys Ser
1 5 10 15
Xaa Ser Cys Val Arg Ser Tyr Cys Thr Leu Phe

20

25

<210> 15
<211> 26
<212> PRT
<213> Conus marmoreus

<220>
<221> PEPTIDE
<222> (1)..(26)
<223> Xaa at residues 8 and 15 are Trp or 6-bromo-Trp;
Xaa at residue 16 is Glu or
gamma-carboxyglutamate.

<400> 15
Asn Gly Gly Cys Lys Ala Thr Xaa Met Ser Cys Ser Ser Gly Xaa Xaa
1 5 10 15
Cys Cys Ser Met Ser Cys Asp Met Tyr Cys
20 25

<210> 16
<211> 323
<212> DNA
<213> Conus textile

<220>
<221> CDS
<222> (1)..(153)

<400> 16
gaa cgg gct aag atc aac ttg ctt cca aag aga aag cca cct gct gag 48
Glu Arg Ala Lys Ile Asn Leu Leu Pro Lys Arg Lys Pro Pro Ala Glu
1 5 10 15
cgt tgg ttg gaa tgc agt gtt tgg ttt tca cat tgt acg aag gac tcg 96
Arg Trp Leu Glu Cys Ser Val Trp Phe Ser His Cys Thr Lys Asp Ser
20 25 30
gaa tgt tgt tct aat agt tgt gac caa acg tac tgc acg tta atg cca 144
Glu Cys Cys Ser Asn Ser Cys Asp Gln Thr Tyr Cys Thr Leu Met Pro
35 40 45
ccg gac tgg tgacatcgcc actctcctgt tcagagtctt caaggctttt 193
Pro Asp Trp
50
gttctctttt gaagaatttt aacgagtga caaaaaagtg gactagcatg tttccttttc 253
cctttgcaaa atcaatgatg gaggtaaaag cctcccat tgtcttcac aataaagaac 313
ttatcatcat 323

<210> 17
<211> 51
<212> PRT
<213> Conus textile

<400> 17
Glu Arg Ala Lys Ile Asn Leu Leu Pro Lys Arg Lys Pro Pro Ala Glu
1 5 10 15

Arg Trp Leu Glu Cys Ser Val Trp Phe Ser His Cys Thr Lys Asp Ser
 20 25 30
 Glu Cys Cys Ser Asn Ser Cys Asp Gln Thr Tyr Cys Thr Leu Met Pro
 35 40 45
 Pro Asp Trp
 50

<210> 18
 <211> 510
 <212> DNA
 <213> Conus textile

<220>
 <221> CDS
 <222> (95)..(337)

<400> 18
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 tctcaacgca cacttgaagt gaaaaacctt tatc atg gag aaa ctg aca att ctg 115
 Met Glu Lys Leu Thr Ile Leu
 1 5
 ctt ctt gtt gct gct gta ctg ttg tcg atc cag gcc cta aat caa gaa 163
 Leu Leu Val Ala Ala Val Leu Leu Ser Ile Gln Ala Leu Asn Gln Glu
 10 15 20
 aaa cac caa cgg gca aag atc aac ttg ctt tca aag aga aag cca cct 211
 Lys His Gln Arg Ala Lys Ile Asn Leu Leu Ser Lys Arg Lys Pro Pro
 25 30 35
 gct gag cgt tgg tgg cgg tgg gga gga tgc atg gct tgg ttt ggg ctt 259
 Ala Glu Arg Trp Trp Arg Trp Gly Gly Cys Met Ala Trp Phe Gly Leu
 40 45 50 55
 tgt tcg agg gac tcg gaa tgt tgt tct aat agt tgt gac gta acg cgc 307
 Cys Ser Arg Asp Ser Glu Cys Cys Ser Asn Ser Cys Asp Val Thr Arg
 60 65 70
 tgc gag tta atg cca ttc cca cca gac tgg tgacatcgac actctcctct 357
 Cys Glu Leu Met Pro Phe Pro Pro Asp Trp
 75 80
 tcagagtctt caaggctttt gttctctttt gaagaatttt tacgagtga caaaaacgtg 417
 gactagcacg tttccttttc cctttgcaaa atcaatgatg gaggtaaaag tgtcccattt 477
 tgtcttcac cataaagaac ttatcatcat aat 510

<210> 19
 <211> 81
 <212> PRT
 <213> Conus textile

<400> 19
 Met Glu Lys Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Leu Ser
 1 5 10 15
 Ile Gln Ala Leu Asn Gln Glu Lys His Gln Arg Ala Lys Ile Asn Leu
 20 25 30

Leu Ser Lys Arg Lys Pro Pro Ala Glu Arg Trp Trp Arg Trp Gly Gly
 35 40 45
 Cys Met Ala Trp Phe Gly Leu Cys Ser Arg Asp Ser Glu Cys Cys Ser
 50 55 60
 Asn Ser Cys Asp Val Thr Arg Cys Glu Leu Met Pro Phe Pro Pro Asp
 65 70 75 80

Trp

<210> 20
 <211> 441
 <212> DNA
 <213> Conus textile

<220>
 <221> CDS
 <222> (16)..(243)

<400> 20
 ggaaaaactt ttatc atg gag aaa ctg aca atc ctg ctc ctt gtt gct gct 51
 Met Glu Lys Leu Thr Ile Leu Leu Leu Val Ala Ala
 1 5 10
 gta ctg atg tcg acc cag gcc atg ttt caa ggt gat gga gaa aaa tcc 99
 Val Leu Met Ser Thr Gln Ala Met Phe Gln Gly Asp Gly Glu Lys Ser
 15 20 25
 cgg aag gcg gag atc aac ttt tct gaa aca aga aag ttg gcg aga aac 147
 Arg Lys Ala Glu Ile Asn Phe Ser Glu Thr Arg Lys Leu Ala Arg Asn
 30 35 40
 aag cag aaa cgc tgc aaa act tat tca aag tat tgt gaa gct gac tcg 195
 Lys Gln Lys Arg Cys Lys Thr Tyr Ser Lys Tyr Cys Glu Ala Asp Ser
 45 50 55 60
 gaa tgc tgt acc gaa cag tgt gta agg tct tac tgc acg ttg ttt gga 243
 Glu Cys Cys Thr Glu Gln Cys Val Arg Ser Tyr Cys Thr Leu Phe Gly
 65 70 75
 tgaattcggg ccacaagcca tccgatatca cccctctcct cttcagaggc ttcaaggctt 303
 ttgttatcct tttgaagaat ctttatcgag taaacataag tagacaagct ttttttttcc 363
 tttgcaaaat gaagaatgat ggcaaaaagc cccccatttt gtcttcatca ataaagaact 423
 cgctatcaga ataaaaaa 441

<210> 21
 <211> 76
 <212> PRT
 <213> Conus textile

<400> 21
 Met Glu Lys Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Met Ser
 1 5 10 15
 Thr Gln Ala Met Phe Gln Gly Asp Gly Glu Lys Ser Arg Lys Ala Glu
 20 25 30
 Ile Asn Phe Ser Glu Thr Arg Lys Leu Ala Arg Asn Lys Gln Lys Arg

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          35              40              45
Cys Lys Thr Tyr Ser Lys Tyr Cys Glu Ala Asp Ser Glu Cys Cys Thr
   50              55              60

Glu Gln Cys Val Arg Ser Tyr Cys Thr Leu Phe Gly
   65              70              75

<210> 22
<211> 460
<212> DNA
<213> Conus textile

<220>
<221> CDS
<222> (49)..(273)

<400> 22
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                                   1

ctg aca att ctg ctt ctt gtt gct gct gtg ctg atg tcg acc cag gcc 105
Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Met Ser Thr Gln Ala
   5              10              15

cta att caa gat caa cgc caa aag gca aag atc aac ttg ttt tca aag 153
Leu Ile Gln Asp Gln Arg Gln Lys Ala Lys Ile Asn Leu Phe Ser Lys
   20              25              30              35

aga cag gca tat gct cgt gat tgg tgg gac gat ggc tgc agt gtg tgg 201
Arg Gln Ala Tyr Ala Arg Asp Trp Trp Asp Asp Gly Cys Ser Val Trp
              40              45              50

ggg cct tgt acg gtg aac gca gaa tgt tgt tct ggt gat tgt cat gaa 249
Gly Pro Cys Thr Val Asn Ala Glu Cys Cys Ser Gly Asp Cys His Glu
              55              60              65

acg tgc att ttc ggg tgg gaa gtc tgaccacaaa ccatccgaca tcgccactct 303
Thr Cys Ile Phe Gly Trp Glu Val
   70              75

cctcttcaga gacttcaagg cttttgttct cttttgaaga attttacgag tgagcaaaaa 363

ggtagactag cacgtttctt tttccctttg caaaatcaat gatggaggta aaagcctccc 423

attttgtcct catcaataaa gaacttatca tcataat 460

<210> 23
<211> 75
<212> PRT
<213> Conus textile

<400> 23
Met Glu Lys Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Met Ser
   1              5              10              15

Thr Gln Ala Leu Ile Gln Asp Gln Arg Gln Lys Ala Lys Ile Asn Leu
   20              25              30

Phe Ser Lys Arg Gln Ala Tyr Ala Arg Asp Trp Trp Asp Asp Gly Cys
   35              40              45

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Ser Val Trp Gly Pro Cys Thr Val Asn Ala Glu Cys Cys Ser Gly Asp
 50 55 60
 Cys His Glu Thr Cys Ile Phe Gly Trp Glu Val
 65 70 75

<210> 24
 <211> 533
 <212> DNA
 <213> Conus textile

<220>
 <221> CDS
 <222> (110)..(337)

<220>
 <221> misc_feature
 <222> (1)..(533)
 <223> n is an unknown nucleotide

<400> 24
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 cctgccgtca tctcagcgca gacttgataa gaagtgaaaa acctttatc atg gag aaa 118
 Met Glu Lys
 1

ctg aca atc ctg ctt ctt gtt gct gct gta ctg atg tcg acc cag gcc 166
 Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Met Ser Thr Gln Ala
 5 10 15

ctg gtt gaa cgt gct gga gaa aac cac tca aag gag aac atc aat ttt 214
 Leu Val Glu Arg Ala Gly Glu Asn His Ser Lys Glu Asn Ile Asn Phe
 20 25 30 35

tta tta aaa aga aag aga gct gct gac agg ggg atg tgg ggc gaa tgc 262
 Leu Leu Lys Arg Lys Arg Ala Ala Asp Arg Gly Met Trp Gly Glu Cys
 40 45 50

aaa gat ggg tta acg aca tgt ttg gcg ccc tca gag tgt tgt tct gag 310
 Lys Asp Gly Leu Thr Thr Cys Leu Ala Pro Ser Glu Cys Cys Ser Glu
 55 60 65

gat tgt gaa ggg agc tgc acg atg tgg tgatgaattc tgaccacaag 357
 Asp Cys Glu Gly Ser Cys Thr Met Trp
 70 75

ccatctgaca tcaccactct cctcttcaga ggcttcaagg cttttgtttt ctttttgaat 417

aatctttacg agtaaacaaa taagtagact agcgcgtttt tttccctttg agaaatcaat 477

gatggaggta aatagcttcc tattttgtct tattcaataa agaacttatc ataata 533

<210> 25
 <211> 76
 <212> PRT
 <213> Conus textile

<400> 25
 Met Glu Lys Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Met Ser
 1 5 10 15

Thr Gln Ala Leu Val Glu Arg Ala Gly Glu Asn His Ser Lys Glu Asn
 20 25 30
 Ile Asn Phe Leu Leu Lys Arg Lys Arg Ala Ala Asp Arg Gly Met*Trp
 35 40 45
 Gly Glu Cys Lys Asp Gly Leu Thr Thr Cys Leu Ala Pro Ser Glu Cys
 50 55 60
 Cys Ser Glu Asp Cys Glu Gly Ser Cys Thr Met Trp
 65 70 75

<210> 26
 <211> 408
 <212> DNA
 <213> Conus gloriamaris

<220>
 <221> CDS
 <222> (2)..(211)

<400> 26
 g ctg aca atc ctg ctt ctt gtt gct gct gta ctg atg tgc acc cag gcc 49
 Leu Thr Ile Leu Leu Val Ala Ala Val Leu Met Ser Thr Gln Ala
 1 5 10 15
 ctg att caa ggt ggt ggt gac aaa cgt caa aag gca aac atc aac ttt 97
 Leu Ile Gln Gly Gly Gly Asp Lys Arg Gln Lys Ala Asn Ile Asn Phe
 20 25 30
 ctt tca agg tgg gac cgt gag tgc agg gct tgg tat gcg ccg tgt agc 145
 Leu Ser Arg Trp Asp Arg Glu Cys Arg Ala Trp Tyr Ala Pro Cys Ser
 35 40 45
 cct ggc gcg caa tgt tgt agt ttg ctg atg tgt tca aaa gcg acc agc 193
 Pro Gly Ala Gln Cys Cys Ser Leu Leu Met Cys Ser Lys Ala Thr Ser
 50 55 60
 cgc tgc ata ttg gcg tta tgaactctga ccacaagcca tccgacatca 241
 Arg Cys Ile Leu Ala Leu
 65 70
 ccactctcct cttcagaggc ttcaaggctt tttgtttttc ttttgaagaa tctttacgag 301
 tgaacaaata agtagaatag cacgtttttc cccctttgca aaatcaataa tggagggttaa 361
 aaaaaaactt ctgtcttctt caataaagaa gttatcataa taaaaaa 408

<210> 27
 <211> 70
 <212> PRT
 <213> Conus gloriamaris

<400> 27
 Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Met Ser Thr Gln Ala
 1 5 10 15
 Leu Ile Gln Gly Gly Gly Asp Lys Arg Gln Lys Ala Asn Ile Asn Phe
 20 25 30
 Leu Ser Arg Trp Asp Arg Glu Cys Arg Ala Trp Tyr Ala Pro Cys Ser
 35 40 45

Pro Gly Ala Gln Cys Cys Ser Leu Leu Met Cys Ser Lys Ala Thr Ser
50 55 60

Arg Cys Ile Leu Ala Leu
65 70

<210> 28
<211> 278
<212> DNA
<213> Conus marmoreus

<220>
<221> CDS
<222> (4)..(222)

<400> 28
atc atg cag aaa ctg ata atc ctg ctt ctt gtt gct gct gtg ctg ctg 48
Met Gln Lys Leu Ile Ile Leu Leu Leu Val Ala Ala Val Leu Leu 15
1 5 10
tcg acc cag gcc cta aat caa gaa aaa cgc cca aag gag atg atc aat 96
Ser Thr Gln Ala Leu Asn Gln Glu Lys Arg Pro Lys Glu Met Ile Asn 30
20 25 30
ttt tta tca aaa gga aag aca aat gct gag agg cgg aac ggc caa tgc 144
Phe Leu Ser Lys Gly Lys Thr Asn Ala Glu Arg Arg Asn Gly Gln Cys 45
35 40 45
gag gat gtt tgg atg cct tgt aca tcg aac tgg gaa tgc tgt tct ttg 192
Glu Asp Val Trp Met Pro Cys Thr Ser Asn Trp Glu Cys Cys Ser Leu 60
50 55 60
gat tgt gaa atg tac tgc aca cag ata gga tgaactctga ccacaagcca 242
Asp Cys Glu Met Tyr Cys Thr Gln Ile Gly 70
65 70
tccgacatca ccactctcct cttcagagtc ttcaag 278

<210> 29
<211> 73
<212> PRT
<213> Conus marmoreus

<400> 29
Met Gln Lys Leu Ile Ile Leu Leu Leu Val Ala Ala Val Leu Leu Ser
1 5 10 15
Thr Gln Ala Leu Asn Gln Glu Lys Arg Pro Lys Glu Met Ile Asn Phe
20 25 30
Leu Ser Lys Gly Lys Thr Asn Ala Glu Arg Arg Asn Gly Gln Cys Glu
35 40 45
Asp Val Trp Met Pro Cys Thr Ser Asn Trp Glu Cys Cys Ser Leu Asp
50 55 60
Cys Glu Met Tyr Cys Thr Gln Ile Gly
65 70

<210> 30
<211> 287

<212> DNA
<213> Conus marmoreus

<220>
<221> CDS
<222> (4)..(231)

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<400> 30
atc atg gag aaa ctg aca atc ctg ctt ctt gtt gct gct gta ctg ata 48
  Met Glu Lys Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Ile
    1                    5                10                15

ccg acc cag gcc ctt ttt caa ggt gat gac gga aaa tcc cag aag gcg 96
Pro Thr Gln Ala Leu Phe Gln Gly Asp Asp Gly Lys Ser Gln Lys Ala
          20                25                30

gag atc aag tct ttt gaa aca aga aag tta gcg aga aac aag cag gta 144
Glu Ile Lys Ser Phe Glu Thr Arg Lys Leu Ala Arg Asn Lys Gln Val
          35                40                45

cgc tgc ggt ggt tgg tca acg tat tgt gaa gtt gac gag gaa tgc tgt 192
Arg Cys Gly Gly Trp Ser Thr Tyr Cys Glu Val Asp Glu Glu Cys Cys
          50                55                60

tcg gaa tca tgt gta agg tct tac tgc acg ctg ttt gga tgaactcgga 241
Ser Glu Ser Cys Val Arg Ser Tyr Cys Thr Leu Phe Gly
    65                70                75

ccacaagcca tccgatatca ccactctcct gttcagagtc ttcaag 287

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<210> 31
<211> 76
<212> PRT
<213> Conus marmoreus

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<400> 31
Met Glu Lys Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Ile Pro
  1                    5                10                15

Thr Gln Ala Leu Phe Gln Gly Asp Asp Gly Lys Ser Gln Lys Ala Glu
          20                25                30

Ile Lys Ser Phe Glu Thr Arg Lys Leu Ala Arg Asn Lys Gln Val Arg
          35                40                45

Cys Gly Gly Trp Ser Thr Tyr Cys Glu Val Asp Glu Glu Cys Cys Ser
          50                55                60

Glu Ser Cys Val Arg Ser Tyr Cys Thr Leu Phe Gly
    65                70                75

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<210> 32
<211> 278
<212> DNA
<213> Conus marmoreus

<220>
<221> CDS
<222> (4)..(213)

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<400> 32
atc atg cag aaa ctg ata att ctg ctt ctt gtt gct gct gtg ctg atg 48

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Met	Gln	Lys	Leu	Ile	Ile	Leu	Leu	Leu	Val	Ala	Ala	Val	Leu	Met		
1				5					10					15		
acg	acc	cag	gcc	cta	tat	caa	gaa	aaa	cgc	cga	aag	gag	atg	atc	aat	96
Thr	Thr	Gln	Ala	Leu	Tyr	Gln	Glu	Lys	Arg	Arg	Lys	Glu	Met	Ile	Asn	
				20					25					30		
ttt	tta	tca	aaa	gga	aag	ata	aat	gct	gag	agg	cgg	aac	ggc	gga	tgc	144
Phe	Leu	Ser	Lys	Gly	Lys	Ile	Asn	Ala	Glu	Arg	Arg	Asn	Gly	Gly	Cys	
			35					40					45			
aaa	gct	act	tg	atg	tct	tgt	tca	tcg	ggc	tg	gaa	tgc	tgt	tct	atg	192
Lys	Ala	Thr	Trp	Met	Ser	Cys	Ser	Ser	Gly	Trp	Glu	Cys	Cys	Ser	Met	
			50				55					60				
agt	tgt	gac	atg	tac	tgc	gga	tagataggat	gaactctgac	cacaagccat							243
Ser	Cys	Asp	Met	Tyr	Cys	Gly										
	65					70										
ccgacatcac	cactctcctc	ttcagagtct	tcaag													278

<210> 33
 <211> 70
 <212> PRT
 <213> Conus marmoreus

Met	Gln	Lys	Leu	Ile	Ile	Leu	Leu	Leu	Val	Ala	Ala	Val	Leu	Met	Thr	
1				5					10					15		
Thr	Gln	Ala	Leu	Tyr	Gln	Glu	Lys	Arg	Arg	Lys	Glu	Met	Ile	Asn	Phe	
			20					25					30			
Leu	Ser	Lys	Gly	Lys	Ile	Asn	Ala	Glu	Arg	Arg	Asn	Gly	Gly	Cys	Lys	
		35					40					45				
Ala	Thr	Trp	Met	Ser	Cys	Ser	Ser	Gly	Trp	Glu	Cys	Cys	Ser	Met	Ser	
	50					55					60					
Cys	Asp	Met	Tyr	Cys	Gly											
	65				70											

<210> 34
 <211> 528
 <212> DNA
 <213> Conus textile

<220>
 <221> CDS
 <222> (98)..(316)

gcacgtcatc	ttctctctca	gtctgcctga	cagctgcctt	cagtcaaccc	tgccgtcatc	60										
tcagcgtaga	cttggtgaaga	agtgaaaaaac	attttatc	atg	cag	aaa	ctg	ata	atc							115
				Met	Gln	Lys	Leu	Ile	Ile							
				1				5								
ctg	ctt	ctt	gtt	gct	gct	gtg	ctg	atg	tcg	acc	cag	gcc	gtg	ctt	caa	163
Leu	Leu	Leu	Val	Ala	Ala	Val	Leu	Met	Ser	Thr	Gln	Ala	Val	Leu	Gln	
			10					15					20			

gaa aaa cgc cca aag gag aag atc aag ctt tta tca aag aga aag aca 211
Glu Lys Arg Pro Lys Glu Lys Ile Lys Leu Leu Ser Lys Arg Lys Thr
25 30 35

gat gct gag aag cag cag aag cgc ctt tgc ccg gat tac acg gag cct 259
Asp Ala Glu Lys Gln Gln Lys Arg Leu Cys Pro Asp Tyr Thr Glu Pro
40 45 50

tgt tca cat gcc cat gaa tgc tgt tca tgg aat tgt tat aat ggg cac 307
Cys Ser His Ala His Glu Cys Cys Ser Trp Asn Cys Tyr Asn Gly His
55 60 65 70

tgt acg gga tgaactcgga ccacaagcca tccgacatca ccactctctct 356
Cys Thr Gly

cttcagaggc ttcaagactt ttgttctgat tttggacaat ctttacgagt aaacaaataa 416

ttagactagc acttttttttc ccctttgcaa aatcaatgat ggaggtaaaa agcctcccat 476

tttgtcttca tcaataaaga acttatcatc aaaaaaaaaa aaaaaaaaaa aa 528

<210> 35

<211> 73

<212> PRT

<213> Conus textile

<400> 35

Met Gln Lys Leu Ile Ile Leu Leu Leu Val Ala Ala Val Leu Met Ser
1 5 10 15

Thr Gln Ala Val Leu Gln Glu Lys Arg Pro Lys Glu Lys Ile Lys Leu
20 25 30

Leu Ser Lys Arg Lys Thr Asp Ala Glu Lys Gln Gln Lys Arg Leu Cys
35 40 45

Pro Asp Tyr Thr Glu Pro Cys Ser His Ala His Glu Cys Cys Ser Trp
50 55 60

Asn Cys Tyr Asn Gly His Cys Thr Gly
65 70

<210> 36

<211> 26

<212> PRT

<213> Conus textile

 $\langle 220 \rangle$

<221> PEPTIDE

<222> (1) .. (26)

<223> Xaa at residue 18 is Trp or 6-bromo-Trp; Xaa at residues 7 and 14 are Glu or gamma-carboxyglutamate; Xaa at residues 3 and 8 are Pro or hydroxy-Pro.

<400> 36

Leu Cys Xaa Asp Tyr Thr Xaa Xaa Cys Ser His Ala His Xaa Cys Cys
1 5 10 15

Ser Xaa Asn Cys Tyr Asn Gly His Cys Thr
20 25

<210> 37
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: consensus
gamma-conopeptide sequence for probe

<220>
<221> PEPTIDE
<222> (1)
<223> Xaa is Glu or Gln.

<400> 37
Xaa Cys Cys Ser
1

<210> 38
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: degenerate
probe for consensus gamma-conopeptide sequence.

<400> 38
sartgytggya gy

12

<210> 39
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: degenerate
probe for consensus gamma-conopeptide sequence.

<220>
<221> misc_feature
<222> (1)..(431)
<223> , n is any nucleotide

<400> 39
sartgytgyt cn

12

<210> 40
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: consensus
pro-gamma-conopeptide sequence for probe.

<400> 40
Ile Leu Leu Val Ala Ala Val Leu
1 5

<210> 41
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: degenerate
 probe for consensus pro-gamma-conopeptide
 sequence.

<220>
 <221> misc_feature
 <222> (1)..(431)
 <223> n is any nucleotide

<400> 41
 athytntyng tngcngcngt nytn

24

<210> 42
 <211> 32
 <212> PRT
 <213> Conus pennaceus

<220>
 <221> PEPTIDE
 <222> (1)..(31)
 <223> Xaa at residues 14 and 26 are
 gamma-carboxyglutamate; Xaa at residue 31 is
 hdroxy-Pro.

<400> 42
 Asp Cys Thr Ser Trp Phe Gly Arg Cys Thr Val Asn Ser Xaa Cys Cys
 1 5 10 15

Ser Asn Ser Cys Asp Gln Thr Tyr Cys Xaa Leu Tyr Ala Phe Xaa Ser
 20 25 30

<210> 43
 <211> 27
 <212> PRT
 <213> Conus textile

<220>
 <221> PEPTIDE
 <222> (1)..(27)
 <223> Xaa at residues 9 and 13 are
 gamma-carboxyglutamate.

<400> 43
 Cys Gly Gly Tyr Ser Thr Tyr Cys Xaa Val Asp Ser Xaa Cys Cys Ser
 1 5 10 15

Asp Asn Cys Val Arg Ser Tyr Cys Thr Leu Phe
 20 25

<210> 44
 <211> 8
 <212> PRT
 <213> Conus pennaceus

<220>
<221> MOD_RES
<222> (2)
<223> Xaa at residue 2 is carboxymethylCys

<400> 44
Asp Xaa Thr Ser Trp Phe Gly Arg
1 5

<210> 45
<211> 24
<212> PRT
<213> Conus pennaceus

<220>
<221> PEPTIDE
<222> (1)..(24)
<223> Xaa at residues 6 and 18 are
gamma-carboxyglutamate; Xaa at residue 23 is
hydroxy-Pro.

<400> 45
Xaa Thr Val Asn Ser Xaa Xaa Xaa Ser Asn Ser Xaa Asp Gln Thr Tyr
1 5 10 15
Xaa Xaa Leu Tyr Ala Phe Xaa Ser
20

<210> 46
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer for M13
universal priming site.

<400> 46
tttcccagtc acgacgtt

18

<210> 47
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer for M13
reverse priming site.

<400> 47
cacacaggaa acagctatg

19